

FIG. 1A

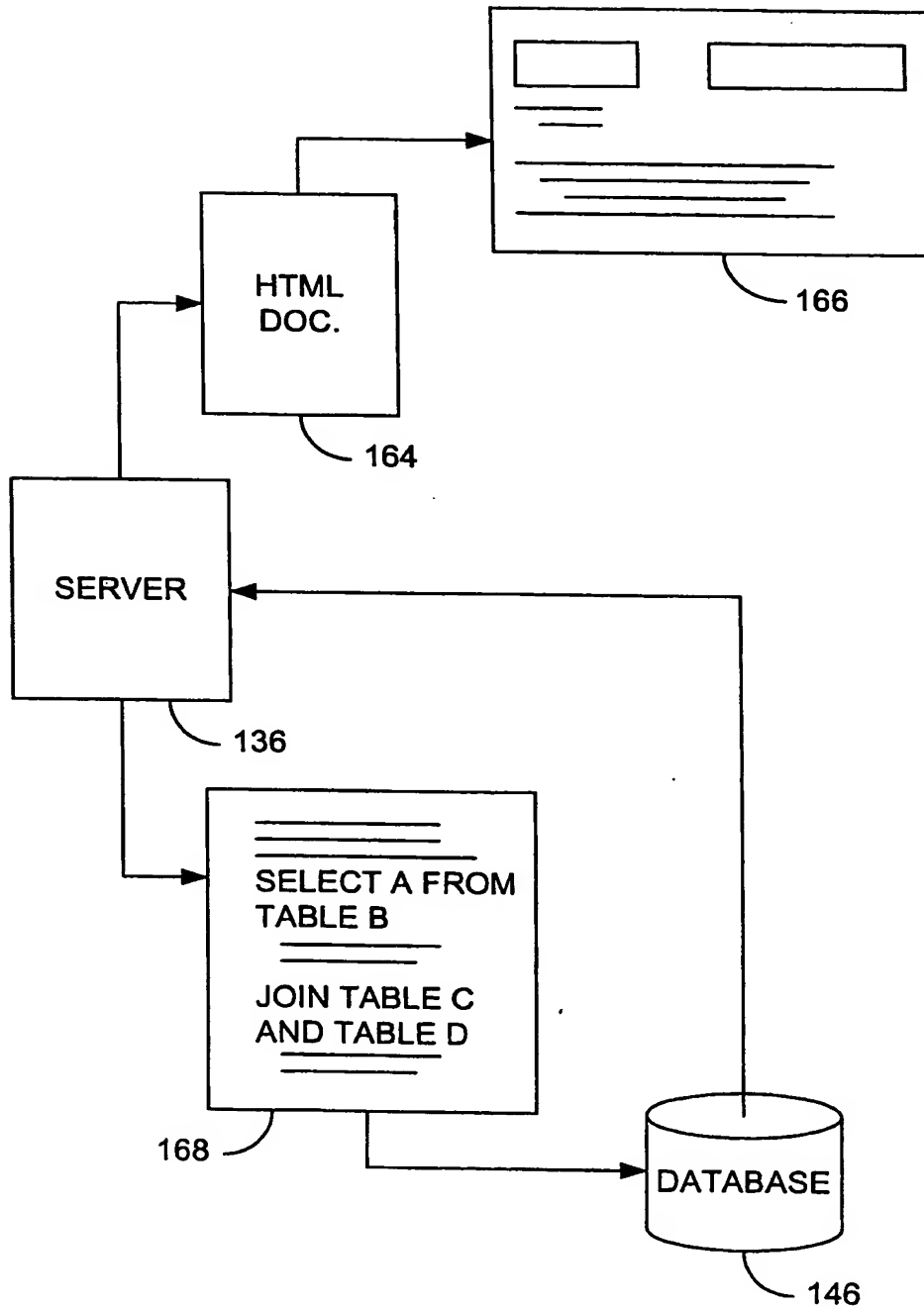


FIG. 1B

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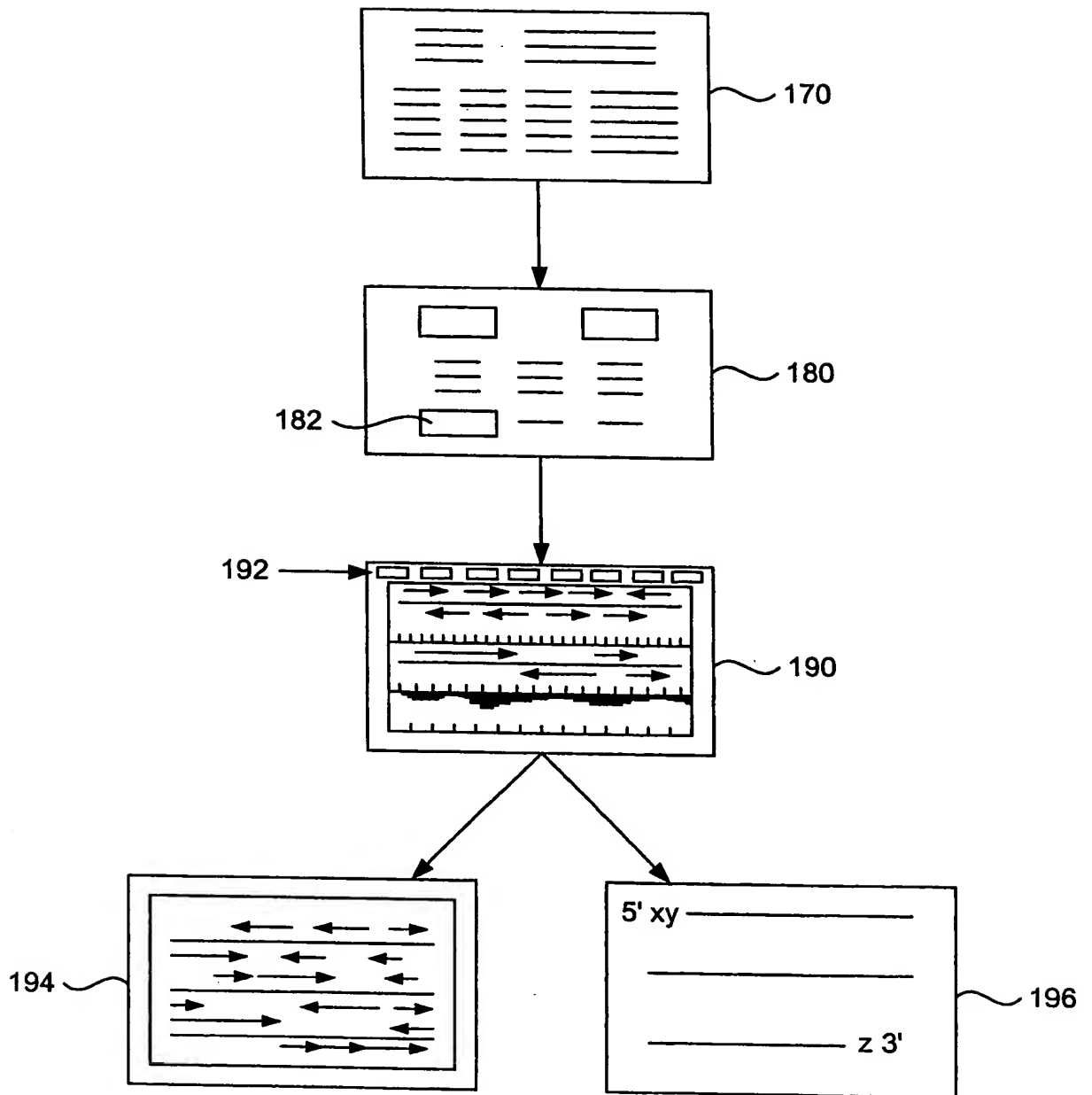


FIG. 1C

Contig Results - Netscape

Contig Results

Main Menu

Org Info

Genome

Contig Summary

Contig

Locus Info

Proteins

Comparisons

Southern

Sequences

Help

Library : SAUREU01

Staphylococcus aureus

Contigs: 48

Contigs ORFs: 134

Contig: SAU1c0039

Length: 138277 bp

Segs: 1846

Base Pairs Selected: 1 to 138277

LocusID	Hit ID	Hit Description	Hit Organism	E-Value	Base Pairs	Libs (48)	Seqs
SAU102730	g2633184	yfh0	Bacillus subtil	3.4e-51	22-2169 (-)	8	26
SAU103442	LUR			1	2170-2722(+)	0	22
SAU100689	g2633977	similar to hypothetical proteins	Bacillus subtil	4.8e-62	2723-3559(+)	24	30
SAU102070	g2633978	ribonuclease H	Bacillus subtil	3.2e-39	3594-4352(+)	34	9
SAU100241	g2462967	putative succinyl-coA synthetase beta ch	Bacillus subtil	6.8e-123	4467-5621(+)	35	13
SAU100242	g2633982	succinyl-CoA synthetase (alpha subunit)	Bacillus subtil	2.9e-97	5655-6542(+)	35	10
SAU102767	g3767593	LyfN	Staphylococcus	4.8e-23	6849-6998(+)	3	7
SAU101151	g3767595	Eph	Staphylococcus	0	7029-8270(+)	13	18
SAU101152	g2633984	ORF4	Staphylococcus	3.5e-109	8514-9314(+)	36	13
SAU101153	g2462971	DNA Topoisomerase I	Bacillus subtil	0	9497-11563(+)	48	32
SAU101154	g2633986	Gid protein	Bacillus subtil	0	11728-13026(+)	43	36
SAU101155	g2633987	integrase/recombinase	Bacillus subtil	7.1e-51	13440-14333(+)	38	27
SAU101156	g2633987	beta-type subunit of the 20S proteasome	Bacillus subtil	9.7e-52	14348-14881(+)	21	17
SAU101157	g2633988	ATP-dependent Cip protease-like	Bacillus subtil	7.4e-95	14971-16350(+)	40	16
SAU101158	g2633989	transcriptional regulator	Bacillus subtil	1.3e-62	16378-17139(+)	9	8
SAU100275	g2634021	ribosomal protein S2	Bacillus subtil	2.8e-73	17493-18200(+)	47	12

FIG. 2

Locus Query - Netscape

Locus Information

Search by LocusID:
 Display: ☒ Locus Details
 ☐ Loci around the selected Locus

~ 302

Locus ID: SAU100241 **Type:** Homology **Gene Category:** Small molecule metabolism
C ntig ID: SAU1c0039 **Position:** 5 of 150
Amino Acids: 385 **Nucleotides:** 1155 **Seqs:** 13
Homologs: 46 **Paralogs:** 1 **Libs:** 35

Top hits: FASTA of ORF against pagenpept110

Hit ID	Hit Description	Hit Organism	E-Value	ORF Coverage
g2462967	putative succinyl-coA synthetase beta ch	Bacillus subtil	6.8e-123	100%
g2633981	succinyl-CoA synthetase (beta subunit)	Bacillus subtil	6.8e-123	100%

FIG. 3

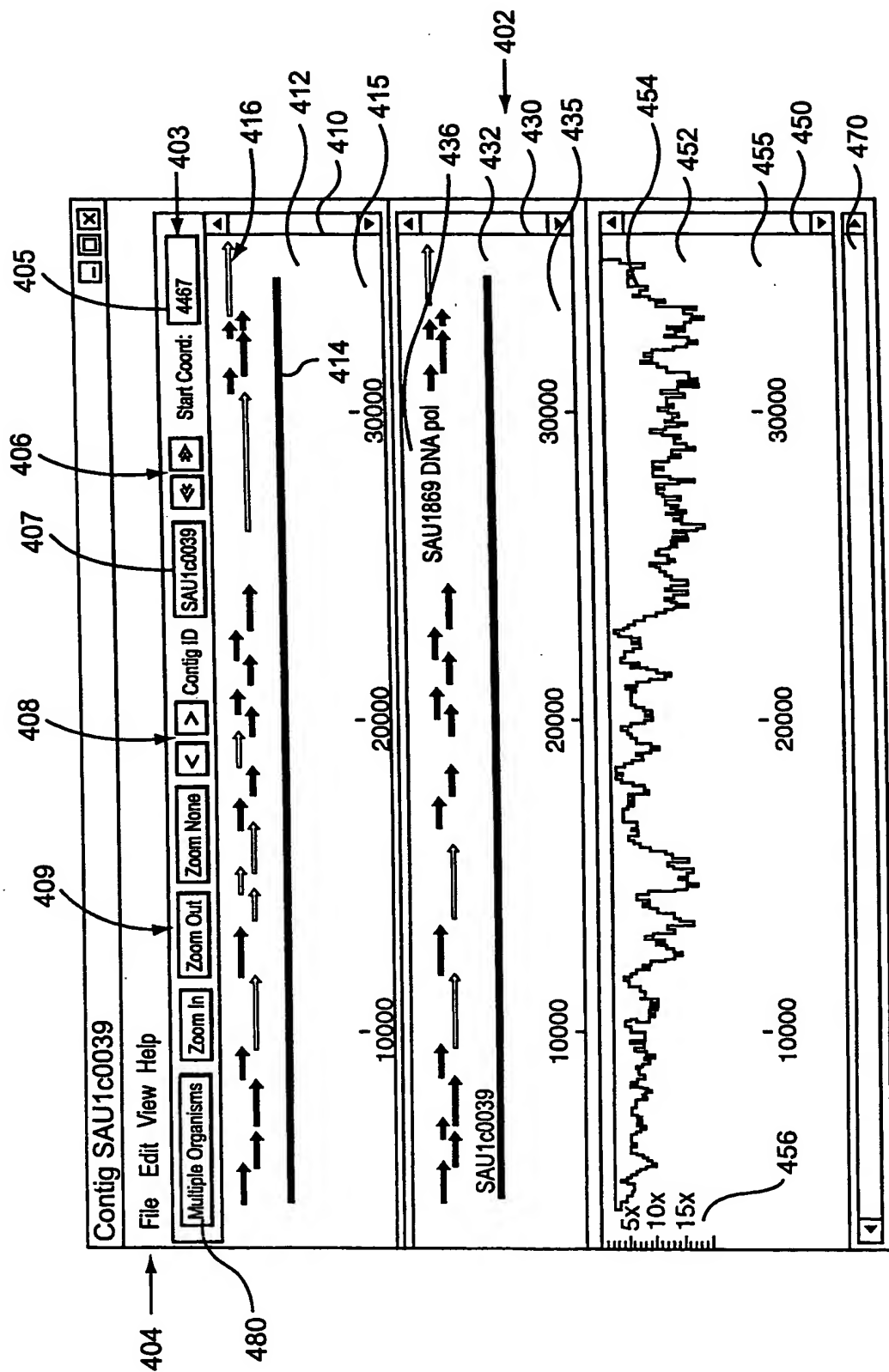


FIG. 4A

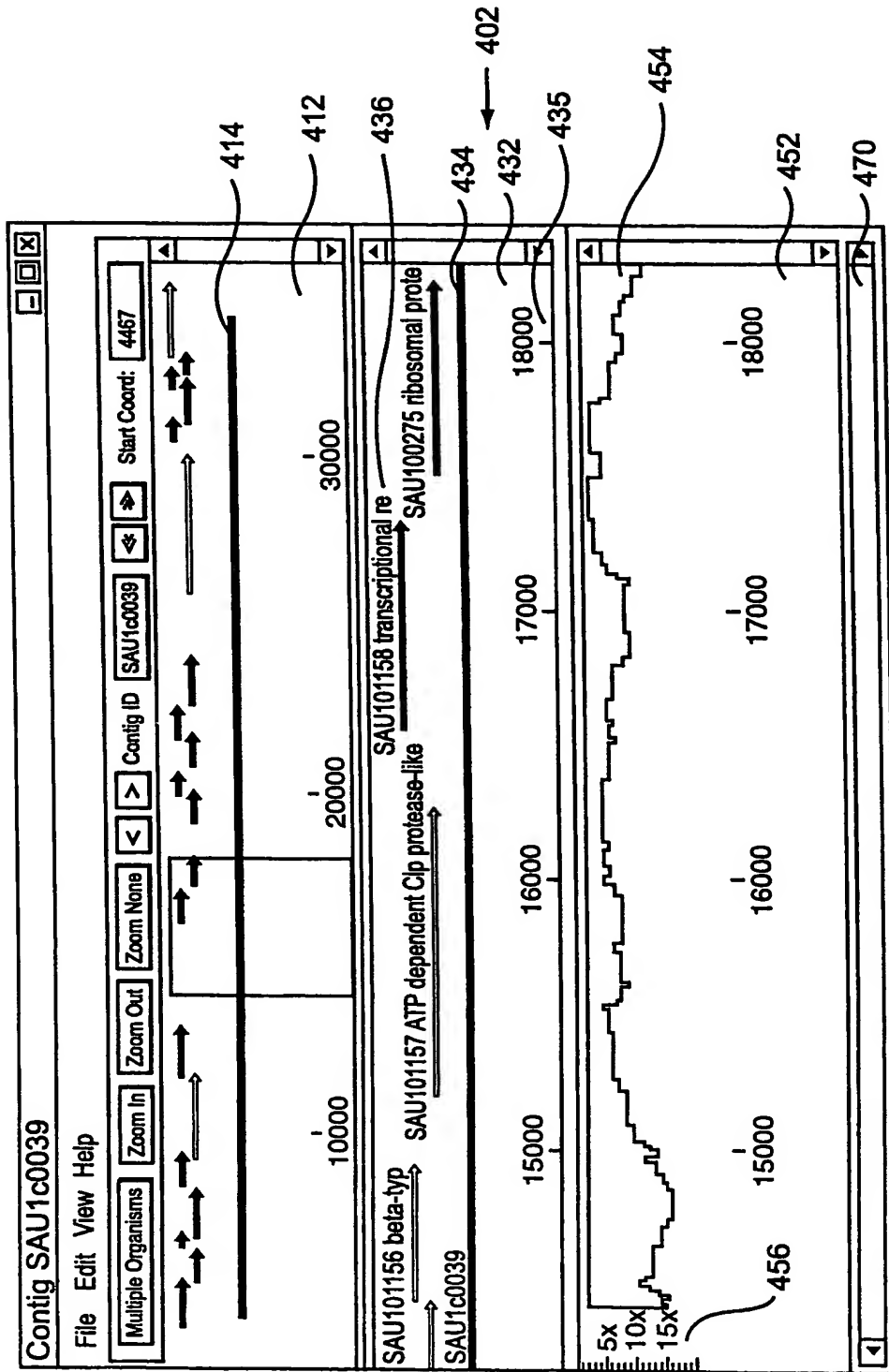


FIG. 4B

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Selected Object Details ✕

Details

Locus ID

Gene Category

Hit Description

EValue

Libs

Seqs

Base Pair

Hit Data Source

Locus Type

HitID1

HitID2

HitID3

HitID4

HitID5

500

502

FIG. 5A

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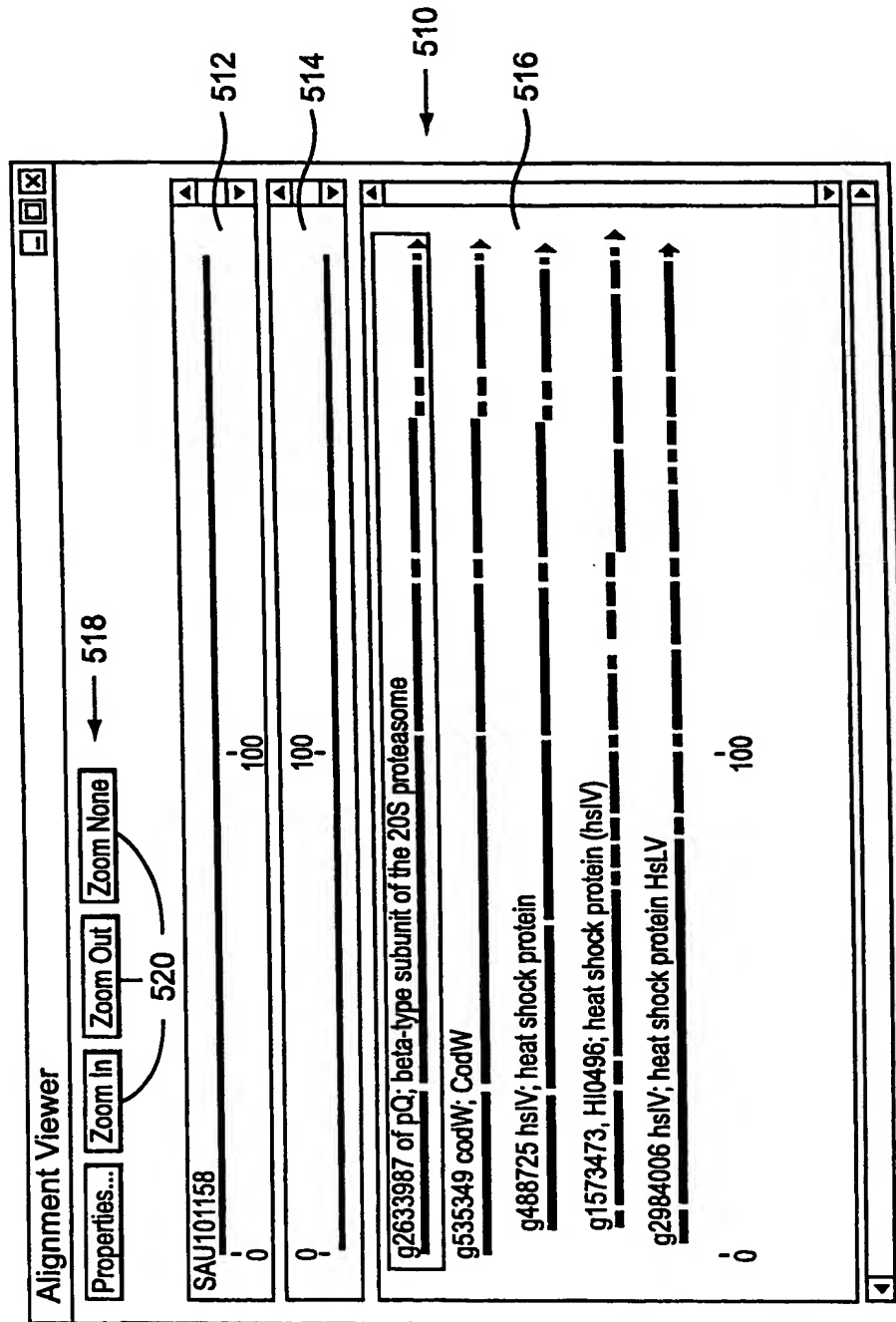


FIG. 5B

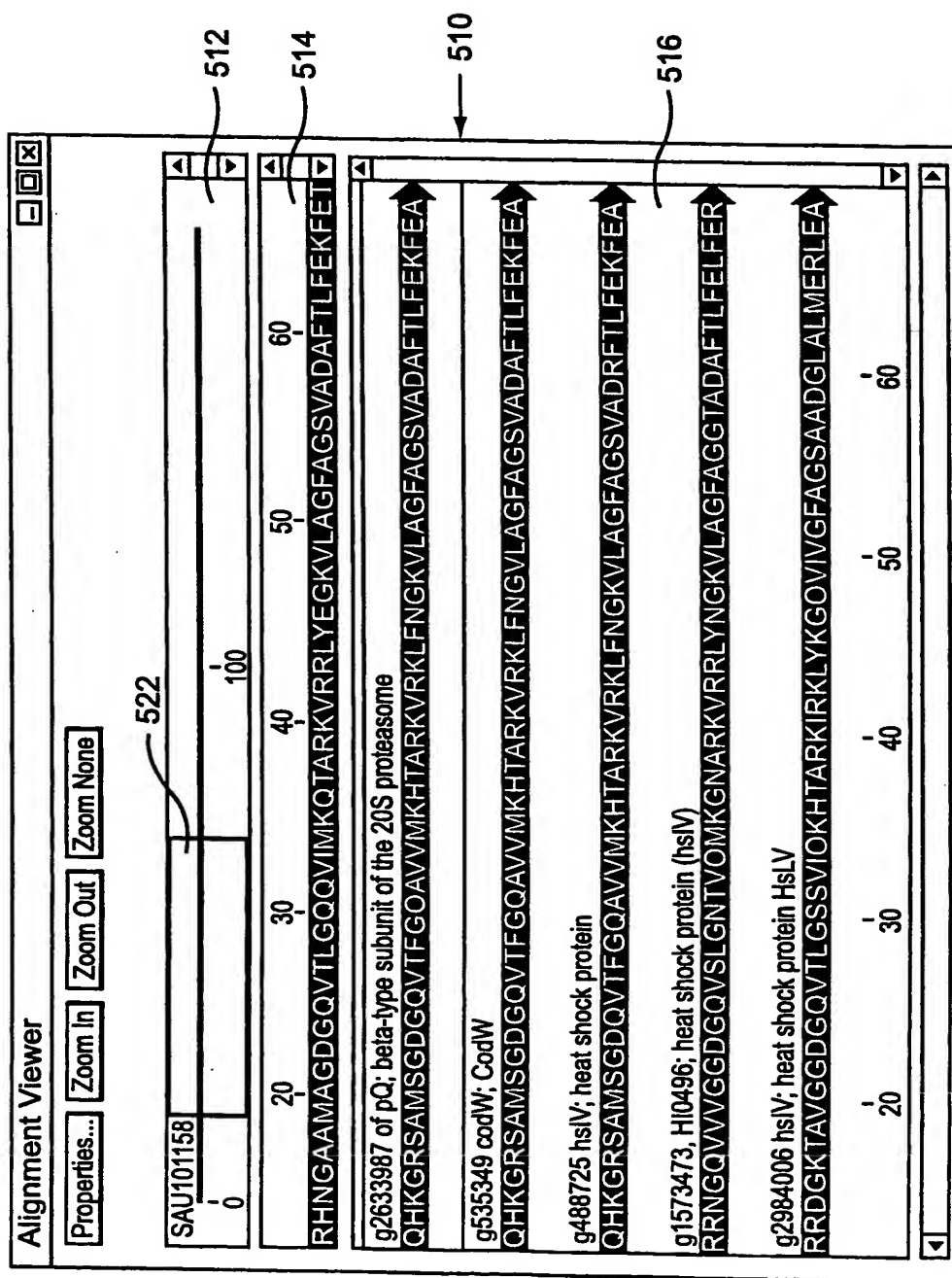


FIG. 5C

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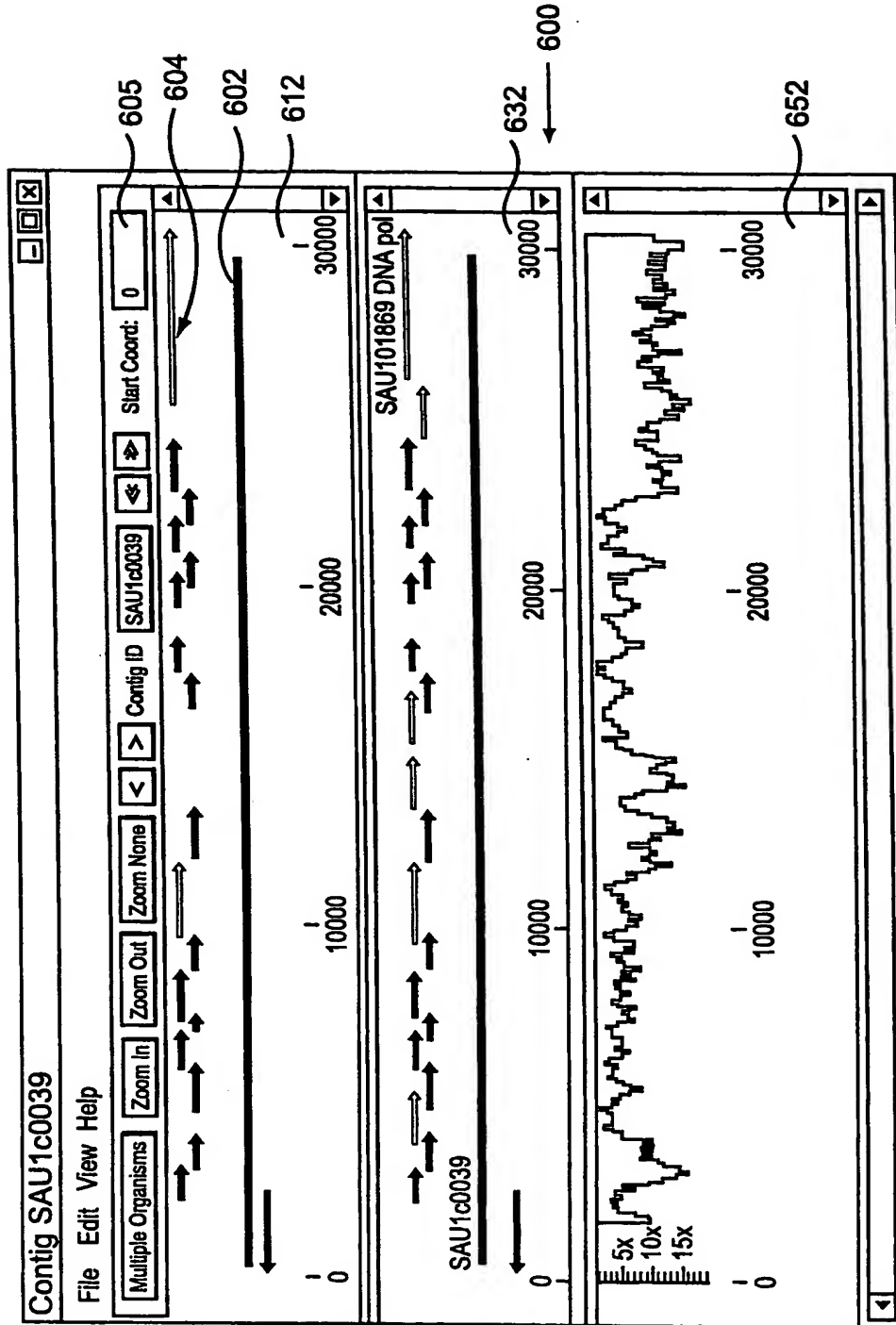


FIG. 6



FIG. 7

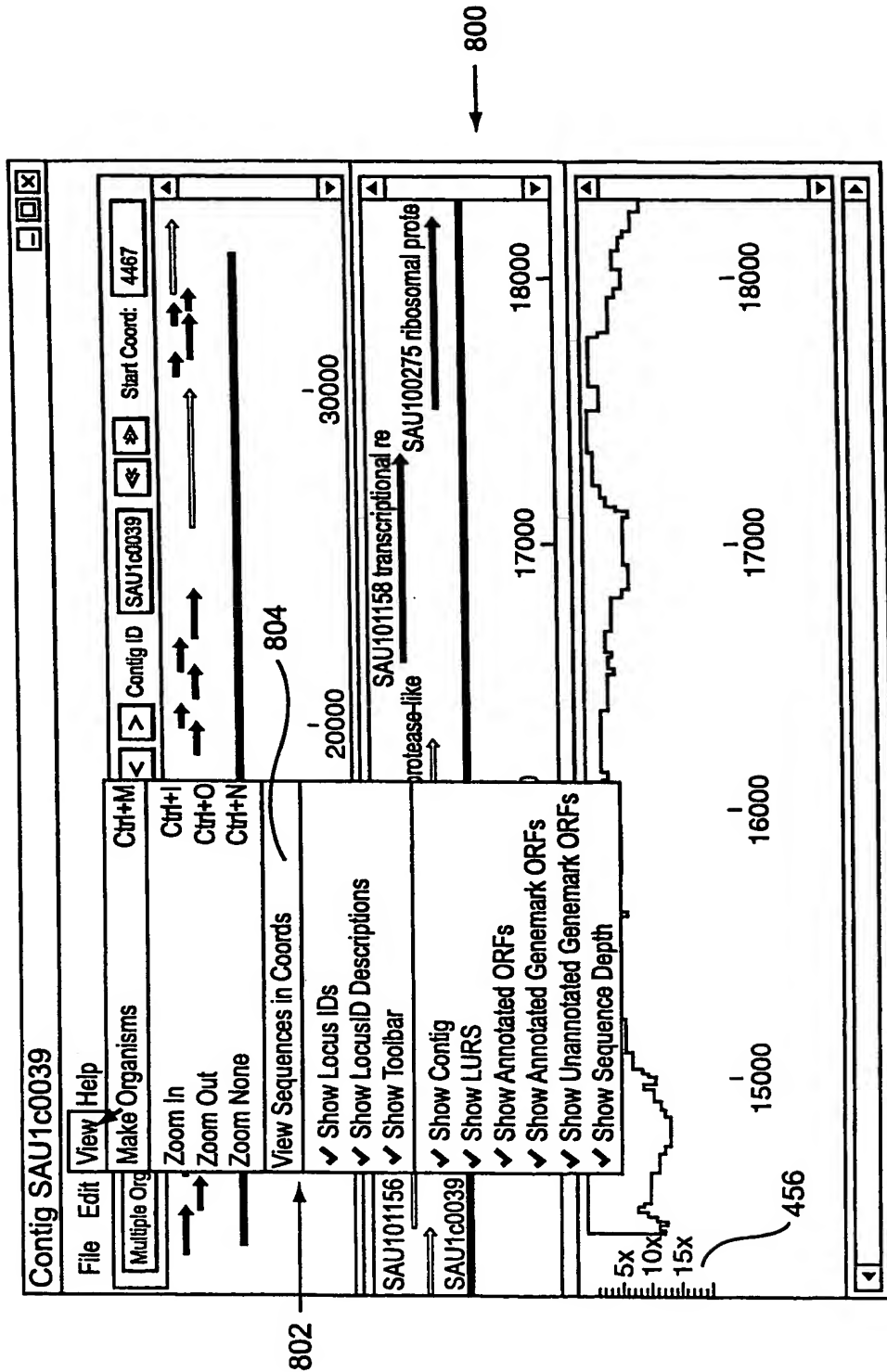


FIG. 8A

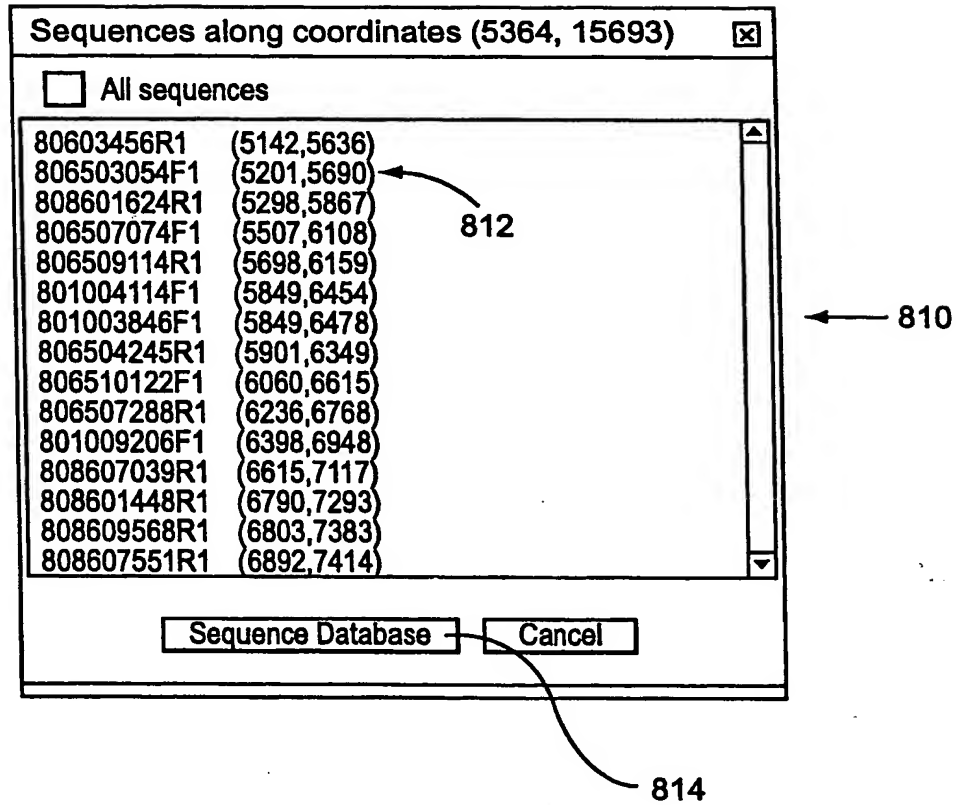
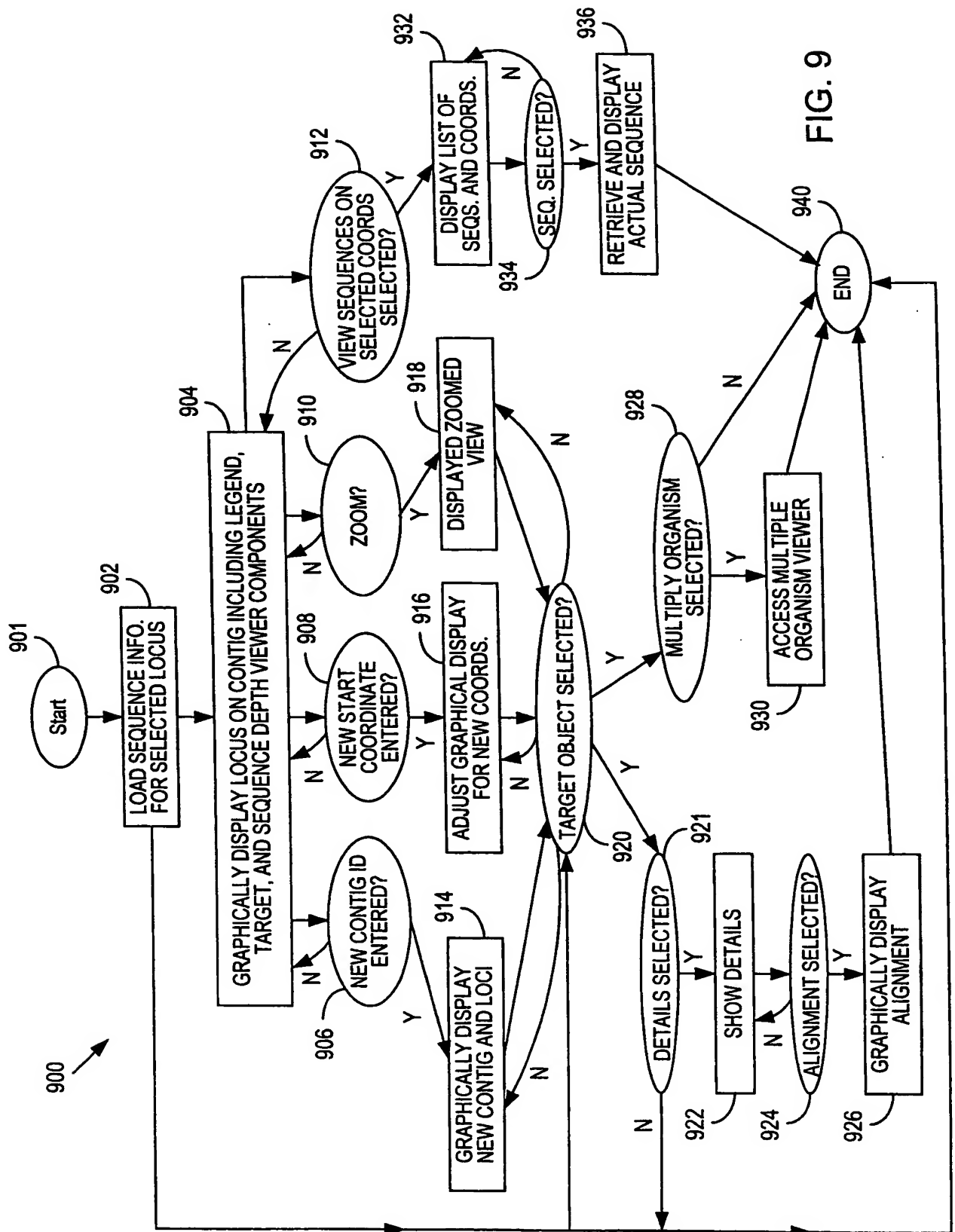


FIG. 8B

[illegible]

FIG. 8C



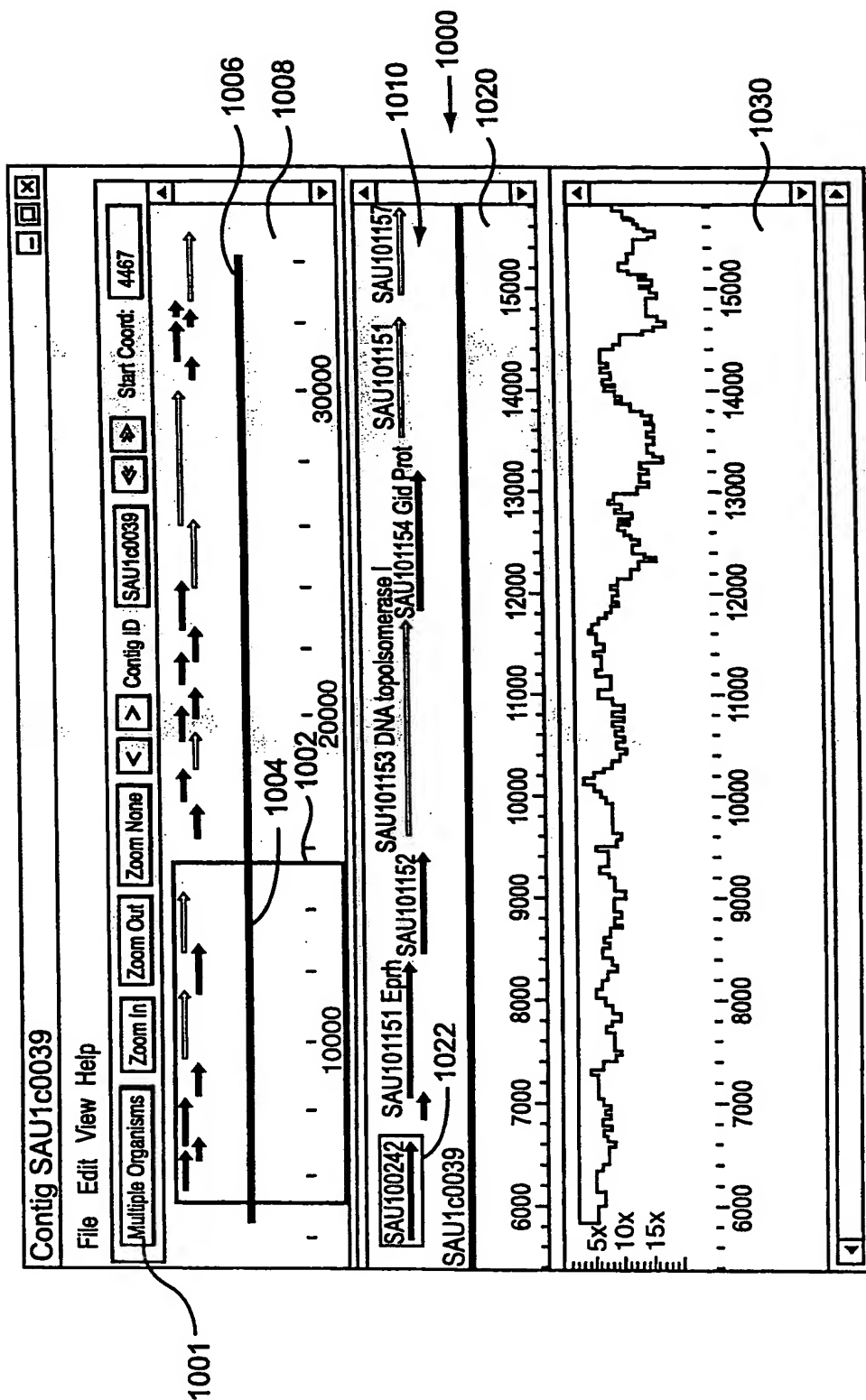


FIG. 10A

Multiple Organism for LocusID - SAU100242 ☒

☐ All Libraries

Paralogs	Library Name
1	SAUREU01 (<i>Staphylococcus aureus</i>)
2	AAEOLI01 (<i>Aquifex aeolicus</i>)
2	AFULGI01 (<i>Archaeoglobus fulgidus</i>)
2	AFUMIG01 (<i>Aspergillus fumigatus</i>)
1	BFARGI01 (<i>Bracteroides fragilis</i>)
1	BPERTU01 (<i>Bordetella pertussis</i>)
1	BSUBTI01 (<i>Bacillus subtilis</i>)
1	CALBIC01 (<i>Candida albicans</i>)
1	CJEJUN01 (<i>Campylobacter jejuni</i>)
1	CPNEUM01 (<i>Chlamydia pneumoniae</i>)
1	CTRACH01 (<i>Chlamydia trachomatis</i>)
1	ECLOAC01 (<i>Enterobacter cloacae</i>)
1	ECOLI01 (<i>Escherichia coli</i>)
3	FGRAMI01 (<i>Fusarium graminearum</i>)

← 1040

1042

FIG. 10B

Multiple Organism for LocusID - SAU100242 [X]

☐ Display all Loci

LocusID	Hit Description
SAU100242	succinyl-CoA synthetase (alpha subunit)
CAL07951	probable succinyl-coa ligase
PRT102068	succinyl-CoA synthetase, alpha subunit
SAU200294	succinyl-CoA synthetase (alpha subunit)
SEP100435	succinyl-CoA synthetase (alpha subunit)
SEP100614	ORF1
SHA100180	succinyl-CoA synthetase (alpha subunit)

Multiple Organism — Cancel

← 1045

1046

FIG. 10C

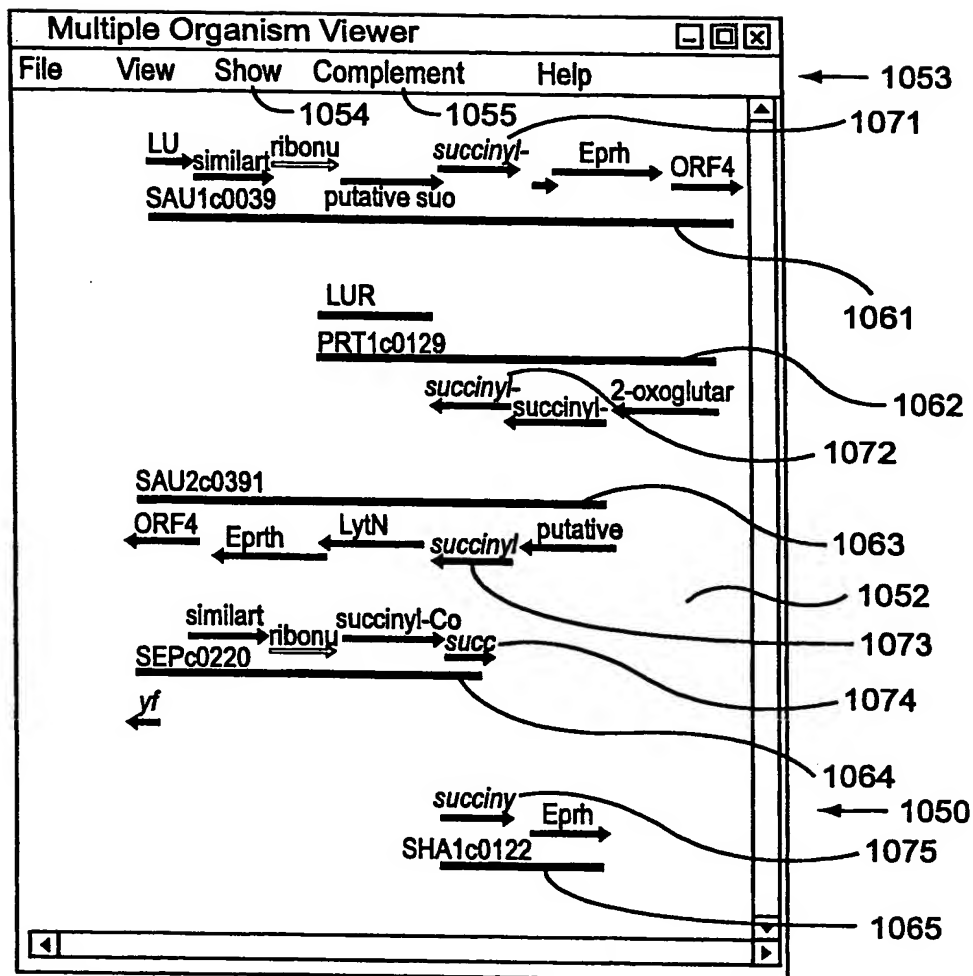


FIG. 10D

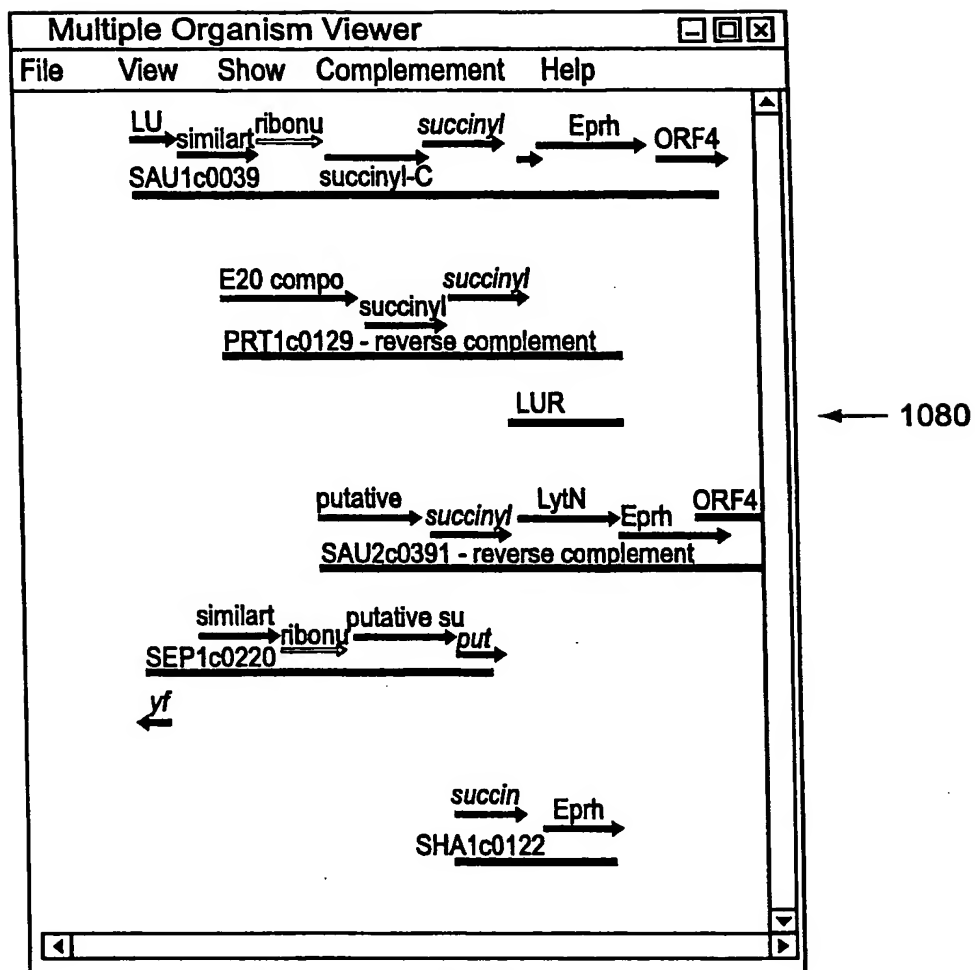


FIG. 10E

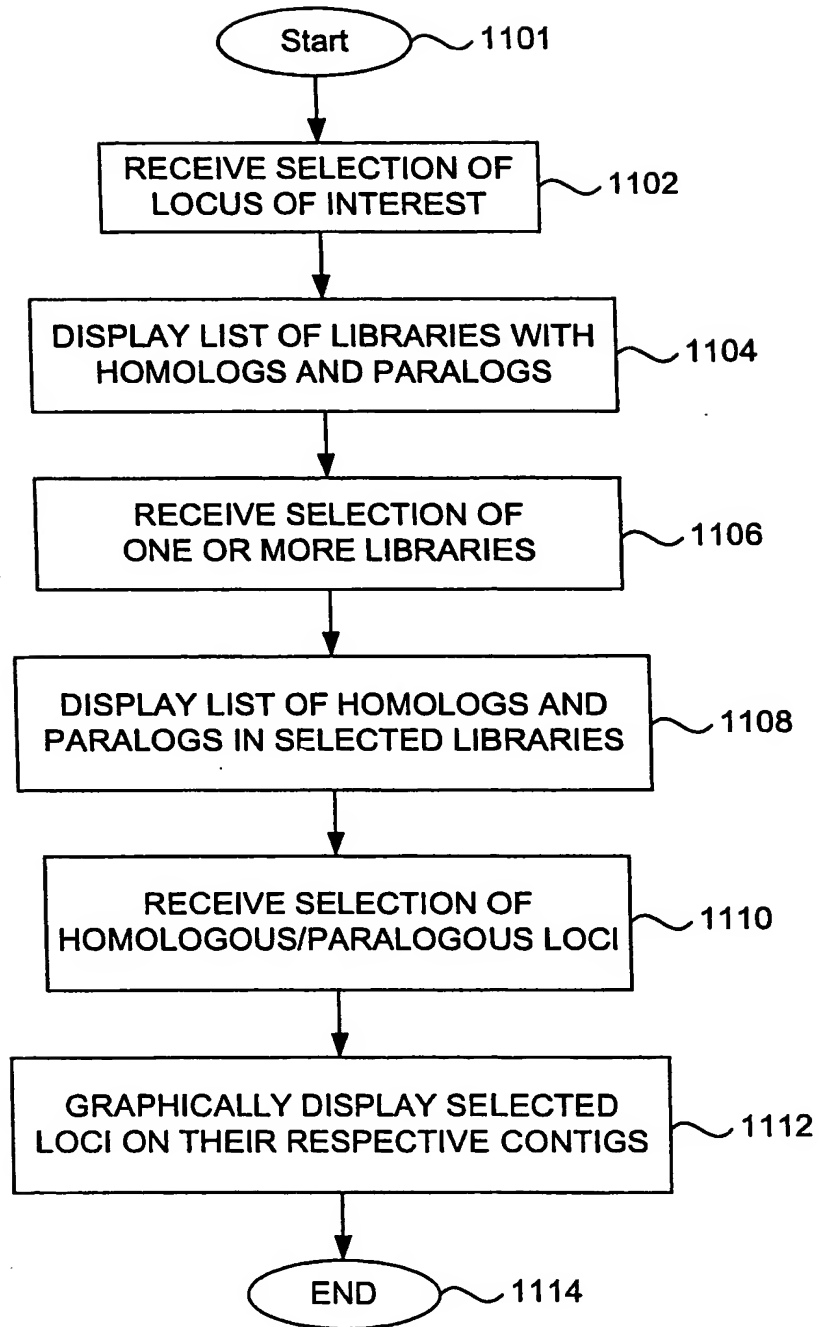


FIG. 11